

Epidemic Computer Simulation

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November 2021

Abstract

Modern network science helped develop a better understanding of how networks work and facilitated the simulation of certain situations. Disease spreading in human societies is a difficult concept to fully understand, given the complexity of the human society network, always changing its morphology. Here we study how disease spreading works by creating a virus spreading computational model, running it in different situations - **with and without quarantine** - and discover the importance of isolating infected agents in a network. This model may help to get a better understanding of the impacts of certain information spreading by running one/multiple simulations on it.

Keywords: Epidemic Model, Computer Simulation

1. Introduction

Since the COVID-19 pandemic, epidemiology became a hot topic. The most common models in disease spreading are the SI model (Susceptible-Infected)[1], the SIS model (Susceptible-Infected-Susceptible)[1], and the SIR model (Susceptible-Infected-Recovered)[1]. They are pretty similar. Therefore, a single model that could run a simulation on each of these models should be a great tool for epidemiologists.

2. Methodology

To create a model that supports the 3 referred models, we must think of the simpler models as particular cases of the more complex ones. Since this model will be run in a network very similar to human society, which is constantly changing, we will omit some network properties that influence the growth of like average path length, average degree, etc... The growth of the epidemic depends mainly on:

SI.

Transmission probability - T .

SIS.

Transmission probability - T .

Recovery time - R . (In SI = infinite)

SIR.

Transmission probability - T .

Recovery time - R . (SI = infinite)

Immunity duration - I . (SIS = 0)

We create a random Watts and Strogatz graph[3] with rewiring probability = 0.5, which is a small world network. In this model, the network will be constantly changing, by isolating infected nodes (quarantine) with probability q during R time steps, or rewiring the edges of nodes connected to infected nodes with probability r of rewiring each edge.

Every time a node gets infected, quarantined or immune, we have to keep record of that time step, to update his state after the duration of the current one. Every node is colored according to this color map:

Susceptible - Grey

Infected - Red

Quarantined - Yellow

Immune - Green

We start by randomly choosing a node to mark as infected. Then, we enter in the given loop:

1. *Each node that's connected to an infected one tries to rewire its edges.*

2. *Change of states of nodes that are no longer in quarantine, infected or immune.*

3. *Each infected node tries to infect his neighbors.*

To better visualize the growth of the epidemic, we color the **first infected node** with **orange**.

3. Results & discussion

We started trying understanding how fast can an epidemic reach its peak when varying the model

parameters by plotting this relations. (Figures 1, 2 and 3)

In Figure 3, it is logical that time to peak should be constant in I , because the immunity is only applicable after the recovery, therefore, it should help preventing the next spreading waves. (Figure 4)

Quarantine: with vs without.

We can see now how quarantine affects the disease spreading figures 5 and 6.

4. Conclusions

With all this in mind, we can say that in most cases, it is more efficient to isolate infected agents, than modifying the virus spread capacity. However, the main goal of this document, was the creation of the model, which can be downloaded [2] and used in related studies to create simulations like the one in figure 7.

References

- [1] R. M. Anderson and R. M. May. *Infectious diseases of humans: dynamics and control*. Oxford university press, 1992.
- [2] D. Barbosa. Epidemic Simulator. <https://github.com/barbosa46/Epidemic-Simulator>, 11 2021.
- [3] D. J. Watts. *Small worlds: The dynamics of networks between order and randomness*. Princeton University Press Princeton, 2000.

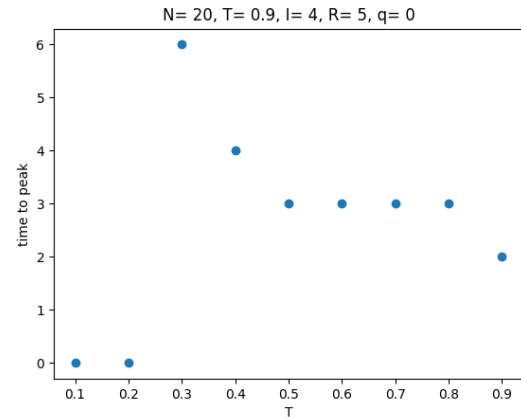


Figure 1: Time to reach 90% of infected for each transmission probability T . 0 means it couldn't reach in decent time. Time to peak tends to decrease exponentially with the increase of T .

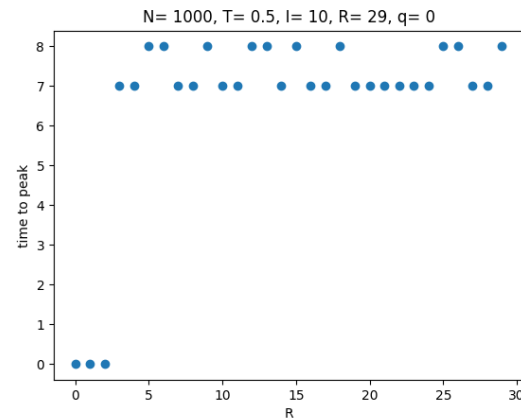


Figure 2: Time to reach 90% of infected for each Recovery duration R . 0 means it couldn't reach in decent time. Time to peak tends to be constant with the increase of R . We can clearly see a threshold for the epidemic to happen. With low values, the epidemic can't spread as fast as the recovery. It doesn't seem to be related with only one of the model parameters.

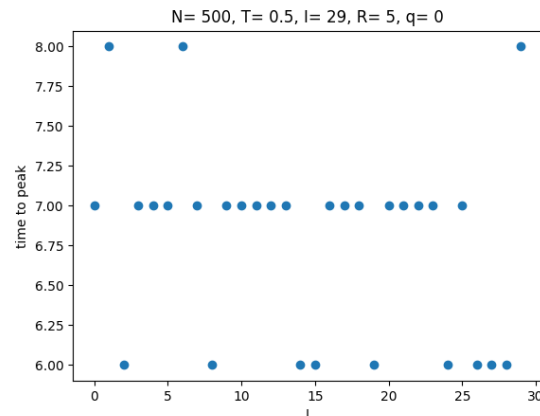


Figure 3: Time to reach 90% of infected for each Immunity duration I . Time to peak tends to be constant with the increase of I .

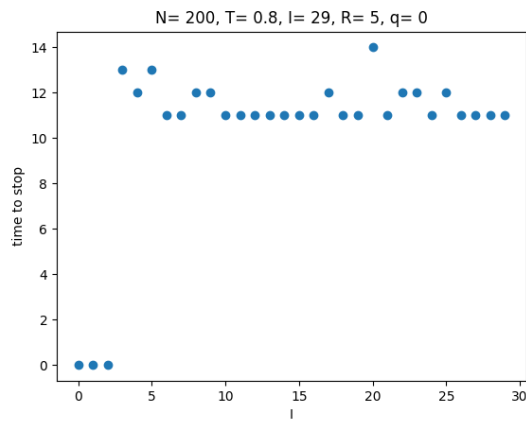


Figure 4: Time to stop the epidemic for each Immunity duration I . 0 means it stop in decent time. Time to stop tends to be constant with the increase of I . We can clearly see a threshold for the epidemic to happen. With low values, the group immunity as fast as the epidemic spreads. It doesn't seem to be related with only one of the model parameters.

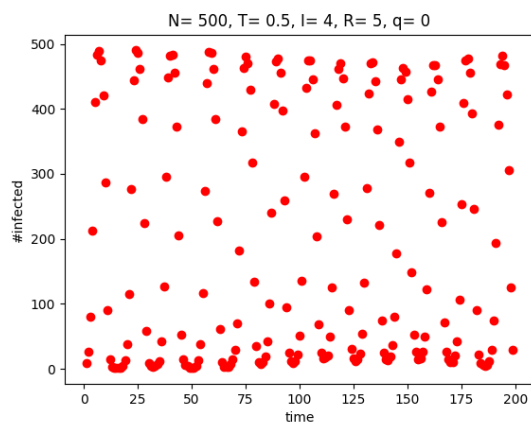


Figure 5: Without quarantine, if the epidemic can't be stopped by itself, it will keep creating infection waves.

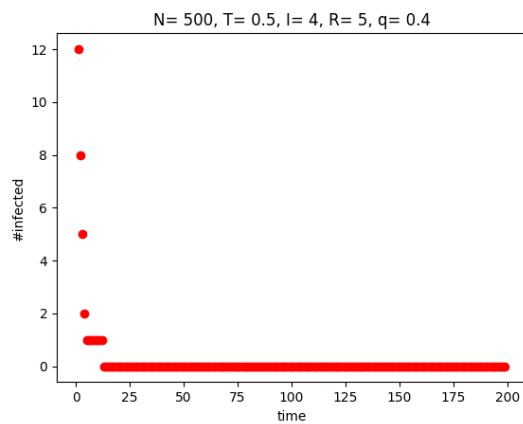


Figure 6: On the other side, with quarantine (probability $q = 40\%$ of putting an infected person in quarantine at each time step), the peak of the infected didn't reached 3% of the population

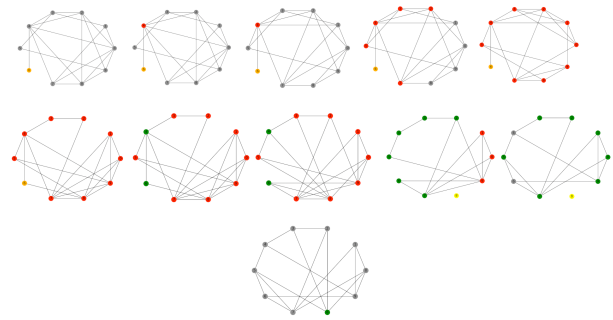


Figure 7: Epidemic Simulation Screenshot sequence